

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/981,421

DATE: 11/02/2001
TIME: 15:08:38

Input Set : A:\3086-A SeqListce filed 101701.txt
Output Set: N:\CRF3\11022001\I981421.raw

ENTERED

3 <110> APPLICANT: Sims, John E.
 4 Mohler, Kendall M.
 5 Born, Teresa L.
 7 <120> TITLE OF INVENTION: METHODS FOR TREATING IL-18 MEDIATED DISORDERS
 9 <130> FILE REFERENCE: 3086-A
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/981,421
 12 <141> CURRENT FILING DATE: 2001-10-17
 14 <150> PRIOR APPLICATION NUMBER: US 60/241,408
 15 <151> PRIOR FILING DATE: 2000-10-18
 17 <160> NUMBER OF SEQ ID NOS: 5
 19 <170> SOFTWARE: PatentIn version 3.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 2681
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Homo sapiens
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (484)..(2283)
 29 <223> OTHER INFORMATION:
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 37 ttatgtctta agagcaggaa ataaaagagac agctgaaggt gtgccttga ccaactgaaa 180
 39 gggaaatctt catcctctga aaaaacatat gtgattctca aaaaacgcac ctggaaaatt 240
 41 gataaagaag cgattctgtt gattctccca gcgcgttgttgg gctctcaatt ccttctgtga 300
 43 aggacaacat atggtgatgg gggaaatcaga agcttgaga ccctctacac ctggatatga 360
 45 atcccccttc taatacttac cagaaaatgaa ggggatactc agggcagagt tctgaatctc 420
 47 aaaacactct actctggcaa aggaatgaaat ttattggagt gatgacagaga acacgggaga 480
 49 aca atg ctc tgt ttg ggc tgg ata ttt ctt tgg ctt gtt gca gga gag 528
 50 Met Leu Cys Leu Gly Trp Ile Phe Leu Trp Leu Val Ala Gly Glu
 51 1 5 10 15
 53 cga att aaa gga ttt aat att tca ggt tgt tcc aca aaa aaa ctc ctt 576
 54 Arg Ile Lys Gly Phe Asn Ile Ser Gly Cys Ser Thr Lys Lys Leu Leu
 55 20 25 30
 57 tgg aca tat tct aca agg agt gaa gag gaa ttt gtc tta ttt tgt gat 624
 58 Trp Thr Tyr Ser Thr Arg Ser Glu Glu Phe Val Leu Phe Cys Asp
 59 35 40 45
 61 tta cca gag cca cag aaa tca cat ttc tgc cac aga aat cga ctc tca 672
 62 Leu Pro Glu Pro Gln Lys Ser His Phe Cys His Arg Asn Arg Leu Ser
 63 50 55 60
 65 cca aaa caa gtc cct gag cac ctg ccc ttc atg ggt agt aac gac cta 720
 66 Pro Lys Gln Val Pro Glu His Leu Pro Phe Met Gly Ser Asn Asp Leu
 67 65 70 75
 69 tct gat gtc caa tgg tac caa caa cct tcg aat gga gat cca tta gag 768
 70 Ser Asp Val Gln Trp Tyr Gln Gln Pro Ser Asn Gly Asp Pro Leu Glu
 71 80 85 90 95
 73 gac att agg aaa agc tat cct cac att cag gac aaa tgt acc ctt 816

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74 Asp Ile Arg Lys Ser Tyr Pro His Ile Ile Gln Asp Lys Cys Thr Leu		
75 100 105 110		
77 cac ttt ttg acc cca ggg gtg aat aat tct ggg tca tat att tgt aga		864
78 His Phe Leu Thr Pro Gly Val Asn Asn Ser Gly Ser Tyr Ile Cys Arg		
79 115 120 125		
81 ccc aag atg att aag agc ccc tat gat gta gcc tgt tgt gtc aag atg		912
82 Pro Lys Met Ile Lys Ser Pro Tyr Asp Val Ala Cys Cys Val Lys Met		
83 130 135 140		
85 att tta gaa gtt aag ccc cag aca aat gca tcc tgt gag tat tcc gca		960
86 Ile Leu Glu Val Lys Pro Gln Thr Asn Ala Ser Cys Glu Tyr Ser Ala		
87 145 150 155		
89 tca cat aag caa gac cta ctt ctt ggg agc act ggc tct att tct tgc		1008
90 Ser His Lys Gln Asp Leu Leu Leu Gly Ser Thr Gly Ser Ile Ser Cys		
91 160 165 170 175		
93 ccc agt ctc agc tgc caa agt gat gca caa agt cca gcg gta acc tgg		1056
94 Pro Ser Leu Ser Cys Gln Ser Asp Ala Gln Ser Pro Ala Val Thr Trp		
95 180 185 190		
97 tac aag aat gga aaa ctc ctc tct gtg gaa agg agc aac cga atc gta		1104
98 Tyr Lys Asn Gly Lys Leu Leu Ser Val Glu Arg Ser Asn Arg Ile Val		
99 195 200 205		
101 gtg gat gaa gtt tat gac tat cac cag ggc aca tat gta tgt gat tac		1152
102 Val Asp Glu Val Tyr Asp Tyr His Gln Gly Thr Tyr Val Cys Asp Tyr		
103 210 215 220		
105 act cag tcg gat act gtg agt tcg tgg aca gtc aga gct gtt gtt caa		1200
106 Thr Gln Ser Asp Thr Val Ser Ser Trp Thr Val Arg Ala Val Val Gln		
107 225 230 235		
109 gtg aga acc att gtg gga gac act aaa ctc aaa cca gat att ctg gat		1248
110 Val Arg Thr Ile Val Gly Asp Thr Lys Leu Lys Pro Asp Ile Leu Asp		
111 240 245 250 255		
113 cct gtc gag gac aca ctg gaa gta gaa ctt gga aag cct tta act att		1296
114 Pro Val Glu Asp Thr Leu Glu Val Glu Leu Gly Lys Pro Leu Thr Ile		
115 260 265 270		
117 agc tgc aaa gca cga ttt ggc ttt gaa agg gtc ttt aac cct gtc ata		1344
118 Ser Cys Lys Ala Arg Phe Gly Phe Glu Arg Val Phe Asn Pro Val Ile		
119 275 280 285		
121 aaa tgg tac atc aaa gat tct gac cta gag tgg gaa gtc tca gta cct		1392
122 Lys Trp Tyr Ile Lys Asp Ser Asp Leu Glu Trp Glu Val Ser Val Pro		
123 290 295 300		
125 gag gcg aaa agt att aaa tcc act tta aag gat gaa atc att gag cgt		1440
126 Glu Ala Lys Ser Ile Lys Ser Thr Leu Lys Asp Glu Ile Ile Glu Arg		
127 305 310 315		
129 aat atc atc ttg gaa aaa gtc act cag cgt gat ctt cgc agg aag ttt		1488
130 Asn Ile Ile Leu Glu Lys Val Thr Gln Arg Asp Leu Arg Arg Lys Phe		
131 320 325 330 335		
133 gtt tgc ttt gtc cag aac tcc att gga aac aca acc cag tcc gtc caa		1536
134 Val Cys Phe Val Gln Asn Ser Ile Gly Asn Thr Thr Gln Ser Val Gln		
135 340 345 350		
137 ctg aaa gaa aag aga gga gtg gtg ctc ctg tac atc ctg ctt ggc acc		1584
138 Leu Lys Glu Lys Arg Gly Val Val Leu Leu Tyr Ile Leu Leu Gly Thr		

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141	atc ggg acc ctg gtg gcc gtg ctg gcg gcg agt gcc ctc ctc tac agg			1632
142	Ile Gly Thr Leu Val Ala Val Leu Ala Ala Ser Ala Leu Leu Tyr Arg			
143	370	375	380	
145	cac tgg att gaa ata gtg ctg ctg tac cgg acc tac cag agc aag gat			1680
146	His Trp Ile Glu Ile Val Leu Leu Tyr Arg Thr Tyr Gln Ser Lys Asp			
147	385	390	395	
149	cag acg ctt ggg gat aaa aag gat ttt gat gct ttc gta tcc tat gca			1728
150	Gln Thr Leu Gly Asp Lys Lys Asp Phe Asp Ala Phe Val Ser Tyr Ala			
151	400	405	410	415
153	aaa tgg agc tct ttt cca agt gag gcc act tca tct ctg agt gaa gaa			1776
154	Lys Trp Ser Ser Phe Pro Ser Glu Ala Thr Ser Ser Leu Ser Glu Glu			
155	420	425	430	
157	cac ttg gcc ctg agc cta ttt cct gat gtt tta gaa aac aaa tat gga			1824
158	His Leu Ala Leu Ser Leu Phe Pro Asp Val Leu Glu Asn Lys Tyr Gly			
159	435	440	445	
161	tat agc ctg tgt ttg ctt gaa aga gat gtg gct cca gga gga gtg tat			1872
162	Tyr Ser Leu Cys Leu Leu Glu Arg Asp Val Ala Pro Gly Gly Val Tyr			
163	450	455	460	
165	gca gaa gac att gtg agc att att aag aga agc aga aga gga ata ttt			1920
166	Ala Glu Asp Ile Val Ser Ile Ile Lys Arg Ser Arg Arg Gly Ile Phe			
167	465	470	475	
169	atc ttg agc ccc aac tat gtc aat gga ccc agt atc ttt gaa cta caa			1968
170	Ile Leu Ser Pro Asn Tyr Val Asn Gly Pro Ser Ile Phe Glu Leu Gln			
171	480	485	490	495
173	gca gca gtg aat ctt gcc ttg gat gat caa aca ctg aaa ctc att tta			2016
174	Ala Ala Val Asn Leu Ala Leu Asp Asp Gln Thr Leu Lys Leu Ile Leu			
175	500	505	510	
177	att aag ttc tgt tac ttc caa gag cca gag tct cta cct cat ctc gtg			2064
178	Ile Lys Phe Cys Tyr Phe Gln Glu Pro Glu Ser Leu Pro His Leu Val			
179	515	520	525	
181	aaa aaa gct ctc agg gtt ttg ccc aca gtt act tgg aga ggc tta aaa			2112
182	Lys Lys Ala Leu Arg Val Leu Pro Thr Val Thr Trp Arg Gly Leu Lys			
183	530	535	540	
185	tca gtt cct ccc aat tct agg ttc tgg gcc aaa atg cgc tac cac atg			2160
186	Ser Val Pro Pro Asn Ser Arg Phe Trp Ala Lys Met Arg Tyr His Met			
187	545	550	555	
189	cct gtg aaa aac tct cag gga ttc acg tgg aac cag ctc aga att acc			2208
190	Pro Val Lys Asn Ser Gln Gly Phe Thr Trp Asn Gln Leu Arg Ile Thr			
191	560	565	570	575
193	tct agg att ttt cag tgg aaa gga ctc agt aga aca gaa acc act ggg			2256
194	Ser Arg Ile Phe Gln Trp Lys Gly Leu Ser Arg Thr Glu Thr Thr Gly			
195	580	585	590	
197	agg agc tcc cag cct aag gaa tgg tga aatgagccct ggagccccct			2303
198	Arg Ser Ser Gln Pro Lys Glu Trp			
199	595			
201	ccagtccagt ccctgggata gagatgttgc tggacagaac tcacagctct gtgtgtgtgt			2363
203	gttcaggctg atagggaaatt caaagagtc tctgccagca ccaagcaagc ttgatggaca			2423
205	atggaatggg attgagactg tggtagag ccttgattt cctggactgg acagacggcg			2483

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207 agtgaattct ctagacccgg ggtactttca gtacacaaca cccctaagat ttcccagtgg 2543
 209 tccgagcaga atcagaaaat acagctactt ctgccttatg gcttaggaaac tgtcatgtct 2603
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 228 20 25 30
 231 Thr Tyr Ser Thr Arg Ser Glu Glu Phe Val Leu Phe Cys Asp Leu
 232 35 40 45
 235 Pro Glu Pro Gln Lys Ser His Phe Cys His Arg Asn Arg Leu Ser Pro
 236 50 55 60
 239 Lys Gln Val Pro Glu His Leu Pro Phe Met Gly Ser Asn Asp Leu Ser
 240 65 70 75 80
 243 Asp Val Gln Trp Tyr Gln Gln Pro Ser Asn Gly Asp Pro Leu Glu Asp
 244 85 90 95
 247 Ile Arg Lys Ser Tyr Pro His Ile Ile Gln Asp Lys Cys Thr Leu His
 248 100 105 110
 251 Phe Leu Thr Pro Gly Val Asn Asn Ser Gly Ser Tyr Ile Cys Arg Pro
 252 115 120 125
 255 Lys Met Ile Lys Ser Pro Tyr Asp Val Ala Cys Cys Val Lys Met Ile
 256 130 135 140
 259 Leu Glu Val Lys Pro Gln Thr Asn Ala Ser Cys Glu Tyr Ser Ala Ser
 260 145 150 155 160
 263 His Lys Gln Asp Leu Leu Leu Gly Ser Thr Gly Ser Ile Ser Cys Pro
 264 165 170 175
 267 Ser Leu Ser Cys Gln Ser Asp Ala Gln Ser Pro Ala Val Thr Trp Tyr
 268 180 185 190
 271 Lys Asn Gly Lys Leu Leu Ser Val Glu Arg Ser Asn Arg Ile Val Val
 272 195 200 205
 275 Asp Glu Val Tyr Asp Tyr His Gln Gly Thr Tyr Val Cys Asp Tyr Thr
 276 210 215 220
 279 Gln Ser Asp Thr Val Ser Ser Trp Thr Val Arg Ala Val Val Gln Val
 280 225 230 235 240
 283 Arg Thr Ile Val Gly Asp Thr Lys Leu Lys Pro Asp Ile Leu Asp Pro
 284 245 250 255
 287 Val Glu Asp Thr Leu Glu Val Glu Leu Gly Lys Pro Leu Thr Ile Ser
 288 260 265 270
 291 Cys Lys Ala Arg Phe Gly Phe Glu Arg Val Phe Asn Pro Val Ile Lys
 292 275 280 285
 295 Trp Tyr Ile Lys Asp Ser Asp Leu Glu Trp Glu Val Ser Val Pro Glu
 296 290 295 300
 299 Ala Lys Ser Ile Lys Ser Thr Leu Lys Asp Glu Ile Ile Glu Arg Asn
 300 305 310 315 320

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308				340				345								350
311	Lys	Glu	Lys	Arg	Gly	Val	Val	Leu	Leu	Tyr	Ile	Leu	Leu	Gly	Thr	Ile
312				355				360								365
315	Gly	Thr	Leu	Val	Ala	Val	Leu	Ala	Ala	Ser	Ala	Leu	Leu	Tyr	Arg	His
316				370				375								380
319	Trp	Ile	Glu	Ile	Val	Leu	Leu	Tyr	Arg	Thr	Tyr	Gln	Ser	Lys	Asp	Gln
320	385				390				395							400
323	Thr	Leu	Gly	Asp	Lys	Lys	Asp	Phe	Asp	Ala	Phe	Val	Ser	Tyr	Ala	Lys
324				405				410								415
327	Trp	Ser	Ser	Phe	Pro	Ser	Glu	Ala	Thr	Ser	Ser	Leu	Ser	Glu	Glu	His
328				420				425								430
331	Leu	Ala	Leu	Ser	Leu	Phe	Pro	Asp	Val	Leu	Glu	Asn	Lys	Tyr	Gly	Tyr
332				435				440								445
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344					485				490							495
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348				500				505								510
351	Lys	Phe	Cys	Tyr	Phe	Gln	Glu	Pro	Glu	Ser	Leu	Pro	His	Leu	Val	Lys
352				515				520								525
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356				530				535								540
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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number